***eLife’s* transparent reporting form**

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**Sample-size estimation**

* You should state whether an appropriate sample size was computed when the study was being designed
* You should state the statistical method of sample size computation and any required assumptions
* If no explicit power analysis was used, you should describe how you decided what sample (replicate) size (number) to use

Please outline where this information can be found within the submission (e.g., sections or figure legends), or explain why this information doesn’t apply to your submission:

No explicit power analysis was used. Prior to Exp. 1, we had no strong prior effect-size estimates and therefore chose a moderately large sample size of N=56 (52 after 4 exclusions). The theoretically critical effect size we obtained in that experiment was relatively large. Therefore, we reduced the sample size to around N=40 for Exp. 2 and 3.

Because Exp. 4 involved actual competition between pairs of subjects we again had no strong prior effect-size estimates and therefore targeted a sample size of 100 (i.e., 94 after excluding 3 pairs).

Given that Exp. 2 and 3 produced large and consistent effect sizes, we reduced the sample for the otherwise comparable, but resource-intensive Exp. 5 (using EEG) to N=25.

**Replicates**

* You should report how often each experiment was performed
* You should include a definition of biological versus technical replication
* The data obtained should be provided and sufficient information should be provided to indicate the number of independent biological and/or technical replicates
* If you encountered any outliers, you should describe how these were handled
* Criteria for exclusion/inclusion of data should be clearly stated
* High-throughput sequence data should be uploaded before submission, with a private link for reviewers provided (these are available from both GEO and ArrayExpress)

Please outline where this information can be found within the submission (e.g., sections or figure legends), or explain why this information doesn’t apply to your submission:

The concepts of technical and biological replication do not readily apply to this study. We conceptually replicated our main pattern of results across five experiments and a total of 215 subjects. .

Data and analyses are available through OSF repository (https://osf.io/j6beq/).  Specifically, the repository contains for each of the five experiments, all trial-by-trial data files, as well as R codes to conduct the reported analyses.  For Experiment 5, we also include all relevant EEG data and analyses codes.

No outliers were excluded. As stated in the *Methods* section under *Participants*: A small number of participants were not able to complete the experimental session within the allotted time and were excluded: 4 participants in Exp. 1 and three pairs (6 participants) in Exp. 4a.

**Statistical reporting**

* Statistical analysis methods should be described and justified
* Raw data should be presented in figures whenever informative to do so (typically when N per group is less than 10)
* For each experiment, you should identify the statistical tests used, exact values of N, definitions of center, methods of multiple test correction, and dispersion and precision measures (e.g., mean, median, SD, SEM, confidence intervals; and, for the major substantive results, a measure of effect size (e.g., Pearson's r, Cohen's d)
* Report exact p-values wherever possible alongside the summary statistics and 95% confidence intervals. These should be reported for all key questions and not only when the p-value is less than 0.05.

Please outline where this information can be found within the submission (e.g., sections or figure legends), or explain why this information doesn’t apply to your submission:

Our general analytic approach is explained in the section *Analytic Approach for Testing Main Prediction*; additional explanations for specific analyses are provided in the Methods section, under *History Analyses* and *EEG Analyses*. Information about specific statistical tests are provided in captions to each figure, including SEM or confidence intervals; sample size information is provided in the *Methods* section under *Participants*. Exact p values are provided wherever feasible and for central result; in some cases, where numbers would provide too much clutter, we present symbols for p-value ranges (Figures 4 and 5).

(For large datasets, or papers with a very large number of statistical tests, you may upload a single table file with tests, Ns, etc., with reference to sections in the manuscript.)

**Group allocation**

* Indicate how samples were allocated into experimental groups (in the case of clinical studies, please specify allocation to treatment method); if randomization was used, please also state if restricted randomization was applied
* Indicate if masking was used during group allocation, data collection and/or data analysis

Please outline where this information can be found within the submission (e.g., sections or figure legends), or explain why this information doesn’t apply to your submission:

We conducted no between-subject manipulations. Therefore, these issues do not apply here.

**Additional data files (“source data”)**

* We encourage you to upload relevant additional data files, such as numerical data that are represented as a graph in a figure, or as a summary table
* Where provided, these should be in the most useful format, and they can be uploaded as “Source data” files linked to a main figure or table
* Include model definition files including the full list of parameters used
* Include code used for data analysis (e.g., R, MatLab)
* Avoid stating that data files are “available upon request”

Please indicate the figures or tables for which source data files have been provided:

Data and codes are included in the OSF repository.